We Claim:

1. A crystal of a 30S subunit having a tetragonal space group $P4_12_12$ with unit cell dimensions of a = 401.375 Å, b = 401.375 Å, c = 175.887 Å.

2. A crystal of a 30S subunit having a tetragonal space group $P4_12_12$ with unit cell dimensions of a = 401.4 Å, b = 401.4 Å, c = 175.9 Å.

3. A crystal of a 30S ribosomal subunit having a resolution better (numerically less) than about 3 Å.

4. A crystal a 30S ribosomal subunit having the structure defined by the co-ordinates of Table 1.

5. A computer-based method of rational drug design which comprises:

providing the structure of a 30S ribosomal subunit as defined by the coordinates of Table 1;

providing the structure of a candidate modulator molecule; and

fitting the structure of the candidate to the structure of the 30S of Table 1.

6. A computer-based method for identifying a potential inhibitor of the 30S ribosome comprising the steps of:

a. employing a three-dimensional structure of 30S, or at least one sub-domain thereof, to characterise at least one active site, the three-dimensional structure being defined by atomic coordinate data according to Table 1; and

b. identifying the potential inhibitor by designing or selecting a compound for interaction with the active site.

7. The method of claim 6 which further comprises:

c. obtaining or synthesising the potential inhibitor;

d. contacting the potential inhibitor with 30S to determine the ability of said inhibitor to interact with the 30S.

8. The method of claim 6 which further comprises:

c. obtaining or synthesising said potential ligand;

d. forming a complex of 30S and said potential ligand; and

e. analysing said complex by X-ray crystallography to determine the ability of said potential ligand to interact with 30S.

9. A method for the determination of the structure of a bacterial 30S from a species other than *T. thermophilus* which method comprises:

(a) crystallising the 30S of said species to obtain a crystal;

(b) performing X-ray crystallography on said crystal to obtain X-ray diffraction data;

(c) providing the structure data of Table 1; and

(d) using molecular replacement to calculate an electron density map of the 30S.

10. A computer system, intended to generate structures and/or perform rational drug design for the 30S ribosome or complexes of the 30S ribosome with a potential modulator, the system containing either (a) atomic coordinate data according to Table 1, said data defining the three-dimensional structure of 30S or at least one sub-domain thereof, or (b) structure factor data for 30S, said structure factor data being derivable from the atomic coordinate data of Table 1.

11. A computer readable media with either (a) atomic coordinate data according to Table 1 recorded thereon, said data defining the three-dimensional structure of the 30S ribosome, at least one atom or at least one sub-domain thereof, or (b) structure factor data for the 30S ribosome recorded thereon, the structure factor data being derivable from the atomic coordinate data of Table 1.